Exhibit 4

NCBI   Entrez   BLAST 2 sequences   BLAST   Example   Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site **Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program [blastn ▼] Matrix [Not Applicable ▼]

Parameters used in BLASTN program only:
Reward for a match: [1]   **Penalty for a mismatch:** [-2]

☐ Use Mega BLAST   Strand option [Both strands ▼]

Open gap [5]   and extension gap [2]   penalties
gap x_dropoff [5]   expect [10.0]   word size [11]   Filter ☑   [Align]

Sequence 1 Enter accession or GI [13027635] or download from file
[Browse...]
or sequence in FASTA format from: [0]   to: [0]

Sequence 2 Enter accession or GI [ ]   or download from file
[Browse...]
or sequence in FASTA format from: [0]   to: [0]

accggaagcgctcagacttggtcg

[Align]   [Clea] [Input]

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html   4/28/2002
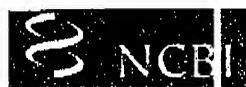
NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   Align

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Sequence 1	gi 13027635	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA	**Length** 2753
Sequence 2	lcl|seq_2		**Length** 25

No significant similarity was found